(19) FRENCH REPUBLIC

NATIONAL INSTITUTE OF INDUSTRIAL PROPERTY

PARIS

(11) **Publication No.:** **2 730 493**
(To be used only in ordering copies)

(21) **National Registration No.** **95 01513**

(51) Int. Cl.[5]: C 07 K 14/16, 1/00, 1/14, C 12 N 15/48, 15/63, 7/00, G 01 N 33/569, A 61 K 39/21, C 07 H 21/00, C 12 Q 1/68

(12) **PATENT APPLICATION** **A1**

(22) **Filing date:** February 9, 1996

(30) **Priority:**

(43) **Date application laid open to the public:** August 14, 1996, Bulletin 96/93.

(56) **List of documents cited in search report:** *See end of this reprint.*

(60) **References to other related national documents:**

(71) **Applicant(s):** INSTITUT PASTEUR -- FR.

(72) **Inventor(s):** MONTAGNIER, LUC; GUETARD, DENISE; COHEN, JACQUES; CHAMARET, SOLANGE; PHILBERT, FREDERIQUE; and TABARY, THIERRY

(73) **Proprietor(s):**

(74) **Representative:** ERNEST GUTMANN YVES PLASSERAUD S.A.

(54) Polypeptides of a transmembrane envelope glycoprotein of the HIV-1 retrovirus and polypeptides having an immunologic relationship therewith

(57) A peptide or polypeptide derived from the MAD HIV-1 deposited with the CNCM under reference designation I-1533 on February 9, 1995, or a polypeptide or peptide, the sequence of which is distinguished from that of the foregoing by the substitution, deletion or addition of amino acids, said different polypeptide or peptide nevertheless retaining the antigenic characteristics of the foregoing.

Polypeptides of a transmembrane envelope glycoprotein of the HIV-1 retrovirus and polypeptides having an immunologic relationship therewith

The instant invention relates to HIV, particularly to a polypeptide and a peptide permitting the detection of anti-HIV antibodies that could not always be detected with the peptides of prior art. The invention is based on the discovery of a new strain of HIV-1, MAD HIV-1. The antiserum directed against this strain has no reactivity whatsoever with the peptides or polypeptides of the HIV consensus as used at this time. The term "HIV consensus" refers to the regions persisting among the isolates, whose detection is essential to the design of vaccines or diagnostic reagents and whose mutations confer resistance to antiviral drugs.

Phylogenic analyses of HIV-1 strains have revealed at least eight subtypes, group O being the must divergent from the HIV-1 consensus (*AIDS Res. Hum. Retroviruses 10* (1994), 877-79).

A general constraint in the development of HIV serologic tests is the need to avoid false positives while at the same time preserving the sensitivity afforded by prior seropositivity detection tests.

Tests based on the use of consensus peptide(s) derived essentially from the *env* gene were considered to be a nearly ideal solution until the discovery of the HIV-1-O variant raised the possibility of false negative results ("Genomic cloning and complete sequence analysis of a highly divergent African human immuno-deficiency virus isolate," *J. Virol. 68* (1994), 1586-96; "A new subtype of human immuno-deficiency virus type 1 (MPV-5180) from Cameroon," *J. Virol. 68* (1994), 1581-85).

The nonreactivity of certain *env* peptide antigen tests in patients who nevertheless exhibit certain clinical syndromes characteristic of AIDS, or lymphadenopathic syndromes that sometimes precede the disease, has occasionally been ascribed to an infection belonging to the O group of HIV-1 ("HIV-1/HIV-2 seronegativity in HIV-1 subtype O infected

patients," *Lancet 343* (1994), 1393-94; "New HIV-1 subtype in the Switzerland [sic]," *Lancet 344* (1994), 270-71).

Unlike group O HIV-1, which is considerably different from the other types of HIV-1, the MAD HIV-1 strain of the instant invention exhibits some sequence homology with the group. However, it still escapes detection by consensus peptides of glycoproteins gp41 and gp120 from this virus.

Hence, the object of the instant invention is to provide diagnostic laboratories with means, particularly specific peptides and polypeptides, for the detection of anti-HIV antibodies that were likely to be undetectable heretofore. It further concerns mixtures of peptides taken from MAD HIV-1 and of peptides corresponding to other HIVs in order to avoid potential "false negative" results.

The invention is based on observations made in an asymptomatic, seropositive woman of Zairan origin in the course of several screening tests for HIV infection, confirmed by Western blot techniques. This patient, however, showed no reactivity to tests based on the recognition of specific *env* peptides of group O HIV-1. Other analyses based on specific peptides demonstrated that her serum reacted only moderately with specific peptides of the HIV-1 group or with peptides of the HIV-1 O group, but reacted with only one peptide from the V3 loop of an African type.

The sequencing of glycoprotein gp41 and the V3 loop of gp120 V3 was performed by means of lymphocytic DNA and viral cultures, indicating that this MAD HIV strain belongs to a portion of the M group of HIV-1 and that it differs significantly from the O group, but without being completely identical to any of the other, already characterized types of HIV-1. In addition, it was found that, at least under the experimental conditions used, which are reported hereinbelow, this strain is not reactive vis-à-vis the consensus peptides of the immunodominant region of gp41, despite the lower number of amino acid substitutions in its peptide sequence compared to the immunodominant regions of other HIV-1 strains.

This observation demonstrates that HIV variants different from group O, although much less distant from the HIV-1 consensus, could still escape serologic detection if such detection were based solely on the consensus peptides expressed by the *env* gene.

The instant invention therefore concerns a polypeptide or a peptide from the MAD

HIV-1 deposited with the CNCM[1] under reference designation I-1533 on February 9, 1995, the genome of which comprises nucleotide sequences that encode the peptide sequences described hereinbelow.

As a variant, the invention concerns a polypeptide or peptide whose sequence is distinguished from that of the foregoing by the substitution, deletion or addition of amino acids, this polypeptide and this peptide nevertheless retaining the antigenic characteristics of the foregoing.

A glycoprotein expressed by the *env* gene of the MAD HIV-1 strain is glycoprotein gp41, a portion of whose peptide sequence and corresponding nucleotide sequence are depicted in Fig. 1B.

Thus, a polypeptide or peptide according to the invention is a polypeptide or peptide containing the peptide sequence shown in Fig. 1B or a peptide portion containing:

a) either the amino acid sequence

RVLAVERYLQDQQLLGIWGCSGKHI

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids in such manner the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or an amino acid sequence according to a) or b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

Preferably, a polypeptide or peptide according to the invention is a polypeptide or peptide characterized in that it contains:

a) either the sequence RVLAVERYLQDQQLLGIWGCSGKHICTTT;

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or a different amino acid sequence according to a) or b) wherein one or more amino

---

[1]TRANSLATOR'S NOTE: *Collection nationale de cultures de micro-organismes*; National Collection of Cultures of Microorganisms.

acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide [of] a).

In a particularly advantageous manner, the polypeptide or peptide is characterized in that it contains:

a) either the sequence RVLAVERYLQDQQLLGIWGCSGKHICTTTVPWNS;

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or a different amino acid sequence according to a) or b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

Another glycoprotein expressed by the *env* gene of the MAD HIV-1 strain is glycoprotein gp120, a portion of whose peptide sequence and corresponding nucleotide sequence are depicted in Fig. 1A.

Thus, the invention is also directed to a polypeptide or peptide containing the sequence shown in Fig. 1A or a portion of this polypeptide containing:

a) either the amino acid sequence QRTGIGPGQALYTTHR,

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or an amino acid sequence according to a) or b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or the peptide of a).

In a preferred manner, this polypeptide or peptide is characterized in that it contains:

a) either the sequence CTRPYKNTRQRTGIGPGQALYTTHRIIGDIRQAHC;

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or an amino acid sequence different from the sequences according to a) and b) wherein one or more amino acids have been deleted or added in such manner that the

polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

The invention is also directed to nucleic acids encoding polypeptides or peptides as defined hereinabove.

One nucleic acid falling within the scope of the invention corresponds to the nucleotide sequence encoding a portion of the peptide sequence of gp41. These two sequences are depicted in Fig. 1B.

Another nucleic acid that also falls within the scope of the instant invention corresponds to the nucleotide sequence encoding a portion of the peptide sequence of gp120. These two sequences are depicted in Fig. 1A.

The invention also pertains to vectors containing a nucleic acid as defined hereinabove.

Thus, vectors according to the invention are plasmids containing the nucleic acids defined hereinabove, as deposited with the CNCM on February 9, 1995, under reference designation

I-1534 for gp120 and _____ for gp41.

The invention is also directed to cells capable of containing a nucleic acid, said nucleic acid conforming to one of the nucleotide sequences as defined hereinabove.

Alternatively, these cells are transfected by means of a vector conforming to the characteristics of a vector described hereinabove.

The instant invention also concerns a virus such as that deposited with the CNCM under reference designation I-1533 on February 9, 1995.

A virus also falling within the scope of the invention is a virus of the same subtype as the foregoing, characterized in that consensus peptides of this virus are recognized by antibodies that also specifically recognize a polypeptide or a peptide defined hereinabove.

The genomic RNA of the virus defined hereinabove also falls within the scope of the invention.

Also falling within the scope of the invention is an outfit or kit for detecting antibodies in the serum or any other biological specimen from a patient who may be infected with HIV-type human retrovirus, characterized in that it comprises:

- at least one polypeptide or peptide whose sequence is one of those described hereinabove;

- means permitting the formation reaction of the immunologic complex between the polypeptide(s) or the peptide(s) and any antibodies that may be present in the biological specimen under test, for example one or more incubating buffers, if needed;

- a negative control specimen;

- means for revealing the antigen/antibody complex formed.

Also according to the invention, said kit further contains at least one consensus polypeptide or peptide derived from another HIV strain or from a polypeptide or peptide comprising

either an amino acid sequence different from the sequence of that polypeptide or peptide, wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the consensus polypeptide or peptide;

or an amino acid sequence wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the consensus polypeptide or peptide.

A kit according to the invention preferably further contains at least one polypeptide or peptide derived from another strain of HIV, preferably the LAI or the MN strain of HIV.

The invention also concerns a polypeptide composition for the *in vitro* diagnosis of an infection caused by the retrovirus according to the invention or by one of its variants, said diagnosis being made in a biological specimen capable of containing the antibodies formed after said infection. This composition is characterized in that it comprises at least one polypeptide or peptide according to the invention.

The biological specimen can be composed in particular of blood, plasma, serum or any other biological extract. The foregoing compositions are usable for detecting antibodies in one of the aforesaid biological specimens.

The invention is therefore also directed to a method for diagnosing *in vitro* an infection due specifically to an HIV-type retrovirus, characterized by the steps of:

- placing a biological specimen capable of containing antibodies produced as the result

of an HIV-1 retrovirus infection in contact with a polypeptide or a peptide conforming to the above definitions, or with a polypeptide or peptide composition described hereinabove, under appropriate conditions permitting the formation of an antigen/antibody type of immunologic complex;

- detection of the complex, if present.

The invention further concerns an immunogenic composition, characterized in that it comprises at least one polypeptide and one peptide in association with a pharmaceutical vehicle acceptable for the making of vaccines.

The invention also relates to a method for the preparation of glycoproteins gp41 and gp120 of the retroviral strain according to the invention, said method being characterized by the following steps:

- lysing cells infected with an HIV-1 retrovirus according to the invention and separating the supernatant and the infected cells, or lysing viral fractions prepared by centrifugation;

- depositing the cellular extract and/or the viral extract on immunoadsorbent containing purified antibodies obtained from serum from a subject infected with the retrovirus according to the invention and advantageously fixed on a suitable substrate, said serum from an infected subject having the ability to react strongly with envelope proteins of the virus according to the invention;

- incubating in the presence of a buffer and for a sufficiently long period of time for an antigen/antibody complex to form;

- washing the immunoadsorbent with a buffer to remove the molecules not retained on the substrate;

- recovering the antigenic proteins sought.

According to a first embodiment of this method of preparation, the separation and recovery of MAD HIV-1 glycoproteins gp41 and gp120 are performed by electrophoresis and by the electroreduction of proteins.

According to another embodiment of this method of preparation, the recovery of the proteins is effected by:

- eluting the proteins fixed on the aforesaid immunoadsorbent;

- purifying the substances so eluted on a chromatography column containing, fixed on the separation substrate, antibodies recognizing MAD HIV-1 glycoprotein gp41 or gp120.

Also falling within the scope of the invention is a method for producing a polypeptide or peptide according to the invention, said polypeptide or peptide being obtained

- either by the expression of a nucleic acid of the invention,

- or by chemical synthesis, by adding amino acids until said polypeptide or peptide is obtained.

The conventional principles and methods of genetic engineering can be used here (*Molecular Cloning*, Sambrook, Fritsch, Maniatis, CSH, 1989).

Also falling within the scope of the invention is a method for producing an above-defined nucleic acid that is producible either by isolation from the virus of the invention or by chemical synthesis, or by using *in vitro* amplification techniques for amplifying nucleic acids with the aid of specific primers.

Thus, the invention also pertains to oligonucleotide primers used in the amplification of nucleic acids encoding oligopeptides of an envelope glycoprotein, for example V3 gp120 glycoprotein from the MAD HIV-1 strain of the instant invention, and of any V3 gp120 sequence from an HIV-1 of group M.

These oligonucleotide primers are characterized in that they possess a sequence comprising at least eight consecutive nucleotides of the following nucleotide sequences:

AATGGCAGTCTAGCAGAAGAA or

TCCTCAGGAGGGGACCCAGAA.

According to the invention, these primers can be used in a method for gene amplification, example by the PCR [polymerase chain reaction] or an equivalent technique, in a nucleotide sequence coding for a peptide of the invention.

The invention also concerns a kit for the above-described amplification by the PCR or an equivalent technique.

Also falling within the scope of the invention is a method for detecting the presence in a biological specimen of nucleic acid(s) characteristic of an HIV retrovirus, including a retrovirus according to the invention. This method comprises placing a DNAc formed from RNA(s) contained in said biological specimen, under conditions permitting the hybridization

of said DNAc, in contact with the retroviral genome and performing gene amplification on this viral specimen.

The invention also concerns a viral lysate such as that obtained by lysing cells infected with a virus according to the invention.

A protein extract of a MAD-HIV strain particularly containing a polypeptide or a peptide as defined hereinabove also falls within the scope of the invention.

Other characteristics and advantages of the invention will emerge from the examples and the figures.

Key to figures

- Fig. 1: superimposition of MAD HIV-1 nucleotide sequences and corresponding encoded peptide sequences;

- Fig. 1A: a fragment of the nucleotide and peptide sequences found in the V3 loop of glycoprotein gp120;

- Fig. 1B: a fragment of the nucleotide and peptide sequences, including the immunodominant region of glycoprotein gp41;

- Fig. 2: a comparison of the amino acid sequences of the V3 loop of glycoprotein gp120 (Fig. 2A) and the immunodominant region of glycoprotein gp41 (Fig. 2B) in different types of HIV-1 strains:

MAD: MAD strain of HIV-1

LAI: BRUCG strain of HIV

OYI: OYI strain of HIV

ELI: ELICG strain of HIV

MAL: MAL strain of HIV

455: 455A strain of HIV

CPZ: CG strain of HIV

ANT: ANT70C strain of HIV

MVP: MVP5518 strain of HIV

VAU: VAU strain of HIV

The sequence CPZ is from a glycoprotein of an SIV strain; ANT, MVP and VAU are

sequences from glycoproteins of strains belonging to the O group of HIV-1.

The amino acid changes with respect to the LAI consensus are shown in bold type when they are found in the sequence of the MAD strain.

Location of some peptides: immunodominant region of gp41 (LAI [***]), ANT (*xxx*), O VMP 5180 [——]).

Example:

DNA sequences from peripheral blood lymphocytes and from viral DNA cultures were obtained by gene amplification of DNA. In the amplification method employed, the inventors used the following nucleotide primers:
CGCGAGCTGCAGTGTTCCTTGGGTTCTTG and
CGCGAGCTGCAGGAGTTTTCCAGAGGAACCCC, as well as
CGCGAGCTGCAGGCGCAACAGCATCTGTTGCAACTC and
CGCGAGCTGCAGTTCTTGTTCATTCTTTTCTTGCTG for the region of glycoprotein gp41, as well as the primers
CGCGAGCTGCAGAATGGCAGTCTAGCAGAAGAA and
CGCGAGCTGCAGTTCTGGGTCCCCTCCTGAGGA for the V3 region of glycoprotein gp120.

All the primers used had in common a 5' end containing a PST1 site permitting subsequent cloning in a Bluescript® plasmid. The products of amplification were either cloned according to the conventional techniques employing the universal primers T3 and T7, or were sequenced directly using the primers from the preceding amplification. The sequences were then determined with the Applied Biosystems 373A automatic sequencing system (ESGS, Montigny le Bretonneux, France).

In a partial sequence of glycoprotein gp41 (MAD strain of HIV-1) encoding 124 amino acids, 11 of them proved to be different from those of the LAI consensus sequence. A comparison of these 11 amino acids in the peptide sequences of the various other strains described hereinabove reveals the following common amino acids:

OYI sequence: 5 amino acids

ELI sequence: 6 amino acids

MAL sequence: 7 amino acids

455 sequence: 7 amino acids

CPZ sequence: 4 amino acids

ANT sequence: 3 amino acids

MPV sequence: 2 amino acids

VAU sequence: 2 amino acids

Although it is less divergent from the LAI consensus sequence than the group O strains, the partial peptide sequence of MAD gp41 nevertheless is not identical to any of those of the other known HIV-1 strains (Fig. 2B).

The serologic reactivity seems to be abolished by only a few amino acid changes in the immunodominant region of glycoprotein gp41. In the case at hand, only four differences were observed in that region (three in each peptide tested). More specifically, the mere replacement of a leucine (the 23rd amino acid in the LAI sequence of Fig. 2) by a histidine, in the small SGKLI loop located between two cysteines, appears to be critical. A specific epitope of the immunodominant region of gp41 in MAD HIV therefore seems to be determined by a single amino acid.

As for the sequence of glycoprotein gp120 including the V3 loop, it is composed of 96 amino acids, 40 of which were found to be different from the LAI consensus sequence.

Some amino acids of the total of 40 in the gp120 sequence from the different strains of Fig. 1A are found in MAD HIV.

OYI sequence: 8 amino acids

ELI sequence: 21 amino acids

MAL sequence: 18 amino acids

455 sequence: 10 amino acids

CPZ sequence: 7 amino acids

ANT sequence: 4 amino acids

MPV sequence: 8 amino acids

VAU sequence: 9 amino acids

The MAD strain of HIV-1 was found to be considerably divergent in sequence from the LAI consensus. Although much closer to the ELI and MAL strains, the MAD strain showed no identity with known HIV-1 strains (Fig. 2); the MAD HIV-1 strain has a GPGQALYT pattern in common with another African strain (MAL HIV-1) in the V3 loop. This common sequence feature is undoubtedly responsible for the serologic cross-reactivities observed.

CLAIMS

1. A peptide or polypeptide derived from the MAD HIV-1 deposited with the CNCM under reference designation I-1533 on February 9, 1995, or a polypeptide or peptide whose sequence is distinguished from that of the foregoing by the substitution, deletion or addition of amino acids, said different polypeptide or peptide nevertheless retaining the antigenic characteristics of the foregoing.

2. A polypeptide or peptide containing the sequence depicted in Fig. 1B or a portion of said polypeptide or peptide containing

a) either the amino acid sequence

RVLAVERYLQDQQLLGIWGCSGKHI

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or the peptide of a),

c) or a different amino acid sequence according to a) or b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

3. A polypeptide or peptide according to claim 2, characterized in that it contains

a) either the sequence RVLAVERYLQDQQLLGIWGCSGKHICTTT

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a),

c) or a different amino acid sequence according to a) and b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

4. A polypeptide or peptide according to claim 2 or 3, characterized in that it contains

a) either the sequence RVLAVERYLQDQQLLGIWGCSGKHICTTTVPWNS;

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or an amino acid sequence different from the sequences according to a) and b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

5. A polypeptide or peptide containing the sequence depicted in Fig. 1A or a portion of said polypeptide or peptide containing:

a) either the amino acid sequence QRTGIGPGQALYTTHR;

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or an amino acid sequence different from the sequences according to a) and b) wherein one or more amino acids have been deleted or added, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

6. A polypeptide or peptide according to claim 5, characterized in that it contains:

a) either the sequence CTRPYKNTRQRTGIGPGQALYTTHRIIGDIRQAHC;

b) or an amino acid sequence different from the sequence of a), wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a);

c) or an amino acid sequence different from the sequences according to a) and b) wherein one or more amino acids have been deleted or added in such manner that the polypeptide or peptide retains its reactivity with an antiserum against the polypeptide or peptide of a).

7. A nucleic acid containing a sequence coding for a polypeptide or peptide according to claims 1 to 6.

8. A nucleic acid according to claim 7 whose nucleotide sequence is depicted in Fig. 1A.

9. A nucleic acid according to claim 7 whose nucleotide sequence is depicted in Fig. 1B.

10. A vector containing a nucleic acid according to any of claims 7 to 9.

11. The vector according to claim 10, characterized in that it is a plasmid.

12. A vector characterized in that it is the plasmid containing the nucleic acid of claim 8 as deposited with the CNCM under reference designation I-1534 on February 9, 1995.

13. A cell containing a nucleic acid according to any of claims 7 to 9 or a vector according to any of claims 10 to 12.

14. The virus deposited with the CNCM under reference designation I-1533 on February 9, 1995.

15. Virus according to claim 14 of the same type or subtype as the virus of claim 14 [sic], characterized in that consensus peptides of said virus are recognized by antibodies specifically recognizing a polypeptide or peptide according to any of claims 1 to 6.

16. The genomic RNA of the virus according to claim 14 or 15.

17. An *in vitro* detection kit for anti-HIV antibodies, containing at least one polypeptide or peptide according to any of claims 1 to 6.

18. The kit according to claim 17, further containing at least one consensus polypeptide or peptide derived from another HIV strain comprising:

either an amino acid sequence different from the sequence of said polypeptide or peptide, wherein one or more amino acids are replaced by other amino acids, provided that the polypeptide or peptide retains its reactivity with an antiserum against said consensus polypeptide or peptide,

or an amino acid sequence wherein one or more amino acids have been deleted or added, provided that said polypeptide or peptide retains its reactivity with an antiserum against said consensus polypeptide or peptide.

19. The kit according to claim 17 or 18, characterized in that the other strain of HIV is an LAI strain of HIV.

20. A polypeptide or peptide composition for the *in vitro* diagnosis of an infection due to the virus according to claim 14 or 15, said composition comprising at least one polypeptide or peptide according to claims 1 to 6.

21. An immunogenic composition characterized in that it comprises at least one polypeptide and one peptide or the peptide in association with a pharmaceutical vehicle acceptable for the making of vaccines.

22. A method for detecting anti-HIV-1 antibodies *in vitro* by placing a biological specimen in contact with a polypeptide or peptide according to any of claims 1 to 6.

23. A method for producing a polypeptide or peptide according to any of claims 1 to 6, characterized in that said polypeptide or peptide is obtained:

- either by the expression of a nucleic acid according to any of claims 7 to 9
- or by chemical synthesis, by adding amino acids until the complete polypeptide or peptide is obtained.

24. An oligonucleotide having a sequence comprising at least eight consecutive nucleotides of the following nucleotide sequences:

AATGGCAGTCTAGCAGAAGAA or

TCCTCAGGAGGGGACCCAGAA.

25. The oligonucleotide according to claim 24, characterized in that it can be used during a gene amplification process performed on a nucleotide sequence coding for a polypeptide or peptide according to any of claims 1 to 6.

26. A kit for gene amplification according to claim 25.

27. A method for detecting the presence in a biological specimen of nucleic acid characteristic of an HIV-type retrovirus, including a retrovirus according to claim 14 or 15, comprising placing a DNAc, formed from RNA(s) contained in said biological specimen under conditions permitting the hybridization of said DNAc, in contact with the retroviral genome and performing gene amplification on said viral specimen.

28. A viral lysate as obtained by the lysis of cells infected with a virus according to claim 14 or 15.

29. A protein extract of the MAD strain of HIV, particularly containing an antigenic polypeptide or peptide according to any of claims 1 to 6.